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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/351,862

DATE: 07/28/1999
TIME: 14:57:22

Input Set: I351862.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: THORPE, PHILIP E.
2 RAN, SOPHIA
3 <120> TITLE OF INVENTION: CANCER TREATMENT KITS USING ANTIBODIES TO
4 AMINOPHOSPHOLIPIDS
5 <130> FILE REFERENCE: 4001.002282
6 <140> CURRENT APPLICATION NUMBER: US/09/351,862
7 <141> CURRENT FILING DATE: 1999-07-12
8 <160> NUMBER OF SEQ ID NOS: 5
9 <170> SOFTWARE: PatentIn Ver. 2.0
10 <210> SEQ ID NO 1
11 <211> LENGTH: 2149
12 <212> TYPE: DNA
13 <213> ORGANISM: Homo sapiens
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17 aaaattttta aattttagaa caaagctaac aaatggctag ttttctatga ttcttcttca 180
18 aacgctttct ttgaggggga aagagtcaaa caaacaagca gttttacctg aaataaagaa 240
19 ctagtttttag aggtcagaag aaaggagcaa gttttgcgag aggcacggaa ggagtgtgct 300
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21 ggggtgcagca atcagcgccg aagtccagaa aacagtggga gaagatataa ccggattcaa 420
22 catgggcaat gtgcctacac tttcattctt ccagaacacg atggcaactg tcgtgagagt 480
23 acgacagacc agtacaacac aaacgctctg cagagagatg ctccacacgt ggaaccggat 540
24 ttctcttccc agaaacttca acatctggaa catgtgatgg aaaattatac tcagtggctg 600
25 caaaaacttg agaattacat tgtggaaaac atgaagtcgg agatggccca gatacagcag 660
26 aatgcagttc agaaccacac ggctaccatg ctggagatag gaaccagcct cctctctcag 720
27 actgcagagc agaccagaaa gctgacagat gttgagaccc aggtactaaa tcaaaactct 780
28 cgacttgaga tacagctgct ggagaattca ttatccacct acaagctaga gaagcaactt 840
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30 atcttagaaa tgaagggaaa acacaaggaa gagttggaca ccttaaagga agagaaagag 960
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52 <211> LENGTH: 498

53 <212> TYPE: PRT

54 <213> ORGANISM: Homo sapiens

55 <400> SEQUENCE: 2

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59 20 25 30
60 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
61 35 40 45
62 Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
63 50 55 60
64 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
65 65 70 75 80
66 Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
67 85 90 95
68 Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
69 100 105 110
70 Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
71 115 120 125
72 Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
73 130 135 140
74 Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
75 145 150 155 160
76 Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
77 165 170 175
78 Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
79 180 185 190
80 Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
81 195 200 205
82 Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
83 210 215 220
84 Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
85 225 230 235 240
86 Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
87 245 250 255
88 Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
89 260 265 270
90 Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
91 275 280 285
92 Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
93 290 295 300
94 Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn

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98      Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
99      340      345      350
100     Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
101     355      360      365
102     Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
103     370      375      380
104     Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
105     385      390      395      400
106     Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
107     405      410      415
108     Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
109     420      425      430
110     Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
111     435      440      445
112     Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
113     450      455      460
114     Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
115     465      470      475      480
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126     agcaggactg ttcttccac tgcaatctga cagtttactg catgcctgga gagaacacag 180
127     cagtaaaaac caggtttgct actggaaaaa gaggaaagag aagactttca ttgacggacc 240
128     cagccatggc agcgtagcag ccctgcgttt cagacggcag cagctcgga ctctggacgt 300
129     gtgtttgccc tcaagtttgc taagctgctg gtttattact gaagaaagaa tgtggcagat 360
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131     gagcatggac agcataggaa agaagcaata tcaggtccag catgggtcct gcagctacac 480
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140     ccaactacag tcaataaaag aagagaaaga tcagctacag gtgttagtat ccaagcaaaa 1020
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148   taatcagcaa cgctatgtgc ttaaaataca ccttaaagac tgggaaggga atgaggctta 1500
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151   cacaaaggat ggagacaacg acaaatgtat ttgcaaatgt tcacaaatgc taacaggagg 1680
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153   gaacacaaat aagttcaacg gcattaaatg gtactactgg aaaggctcag gctattcgct 1800
154   caaggccaca accatgatga tccgaccagc agatttctaa acatcccagt ccactgagg 1860
155   aactgtctcg aactattttc aaagacttaa gccagtgca ctgaaagtca cggctgcgca 1920
156   ctgtgtcctc ttccaccaca gagggcgtgt gtcggtgct gacgggaccc acatgctcca 1980
157   gattagagcc tgtaaaacttt atcacttaaa cttgcatcac ttaacggacc aaagcaagac 2040
158   cctaaacatc cataattgtg attagacaga acacctatgc aaagatgaac ccgaggctga 2100
159   gaatcagact gacagtttac agacgtgct gtcacaacca agaattgtat gtgaagttt 2160
160   atcagtaaat aactggaaaa cagaacactt atgttatata atacagatca tcttggaaat 2220
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<212> TYPE: PRT

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<400> SEQUENCE: 4

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170               20             25             30
171   Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
172               35             40             45
173   Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
174       50             55             60
175   Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
176       65             70             75             80
177   Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
178               85             90             95
179   Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
180               100            105            110
181   Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
182               115            120            125
183   Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
184       130            135            140
185   Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
186       145            150            155            160
187   Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp
188               165            170            175
189   Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
190               180            185            190
191   Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
192               195            200            205
193   Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
194       210            215            220

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198                               245                               250                               255
199   Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ser Ala Lys Asp Pro Thr
200                               260                               265                               270
201   Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe
202                               275                               280                               285
203   Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn
204                               290                               295                               300
205   Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly Gly
206   305                               310                               315                               320
207   Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln
208                               325                               330                               335
209   Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu
210                               340                               345                               350
211   Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg
212                               355                               360                               365
213   Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr
214                               370                               375                               380
215   Ser Leu Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg
216   385                               390                               395                               400
217   Ile His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile
218                               405                               410                               415
219   Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys
220                               420                               425                               430
221   Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp
222                               435                               440                               445
223   Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln
224                               450                               455                               460
225   Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser
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237                               20                               25                               30
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239       35                               40                               45
240   Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
241       50                               55                               60
242   Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Phe Ser Ser Gln Lys Leu
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244   Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp Leu Gln Lys

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